

FIG. 1

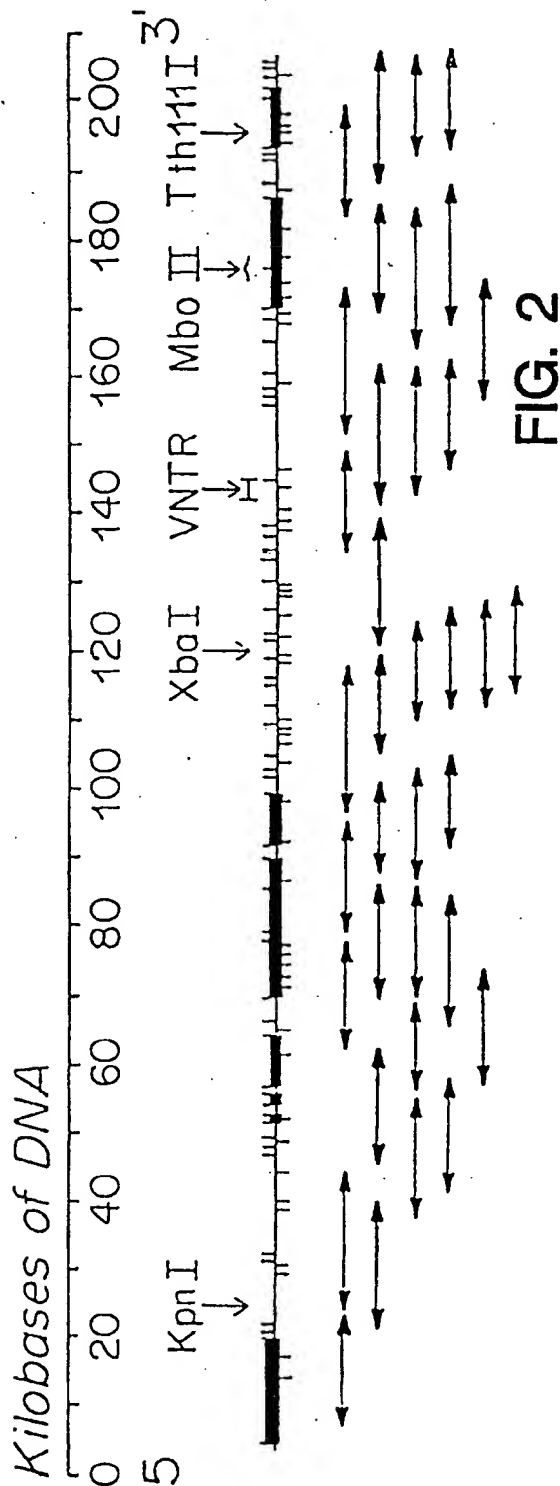


FIG. 2

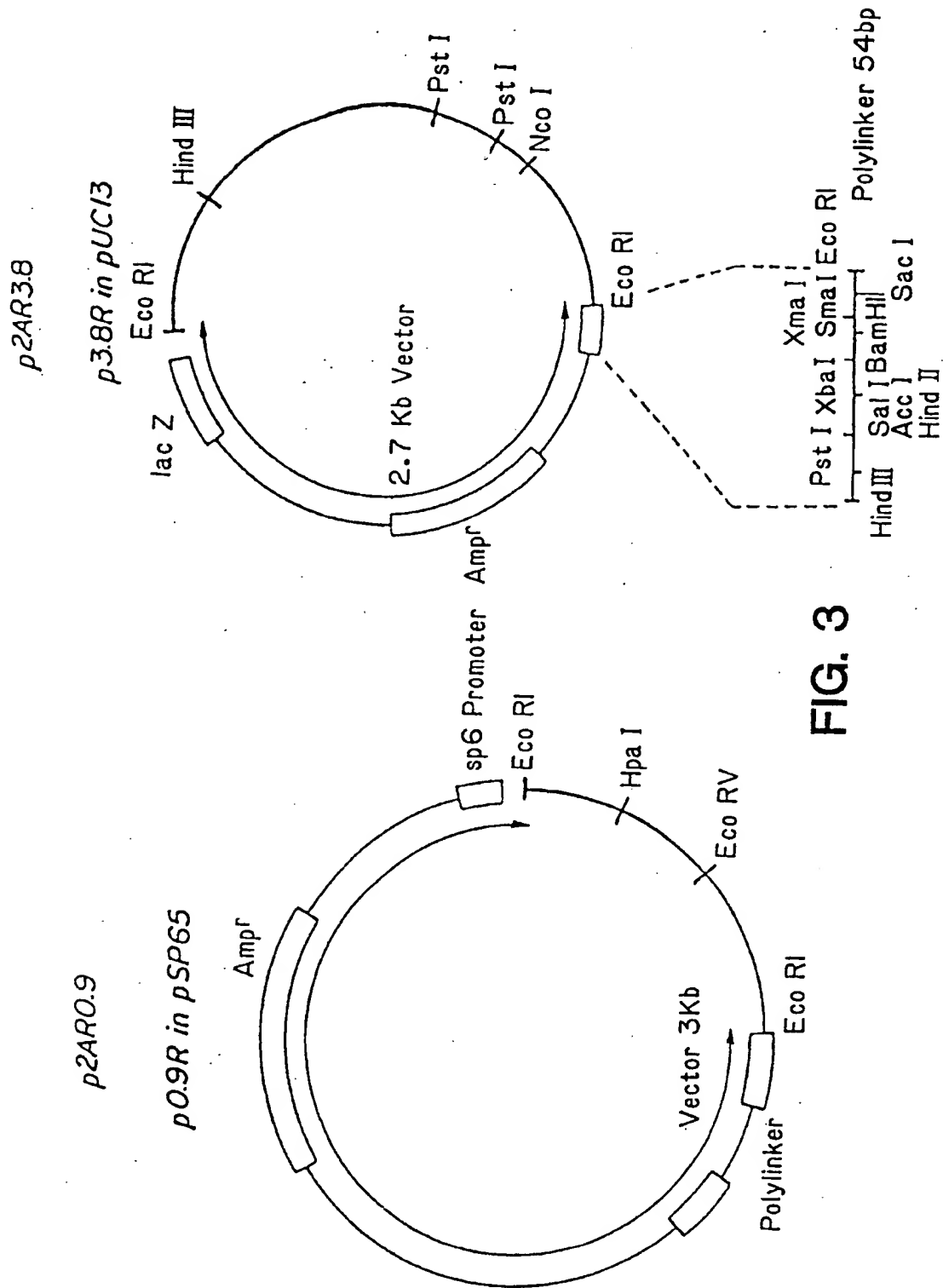


FIG. 3

FIG. 4

MAP OF THE RETINOBLASTOMA GENE

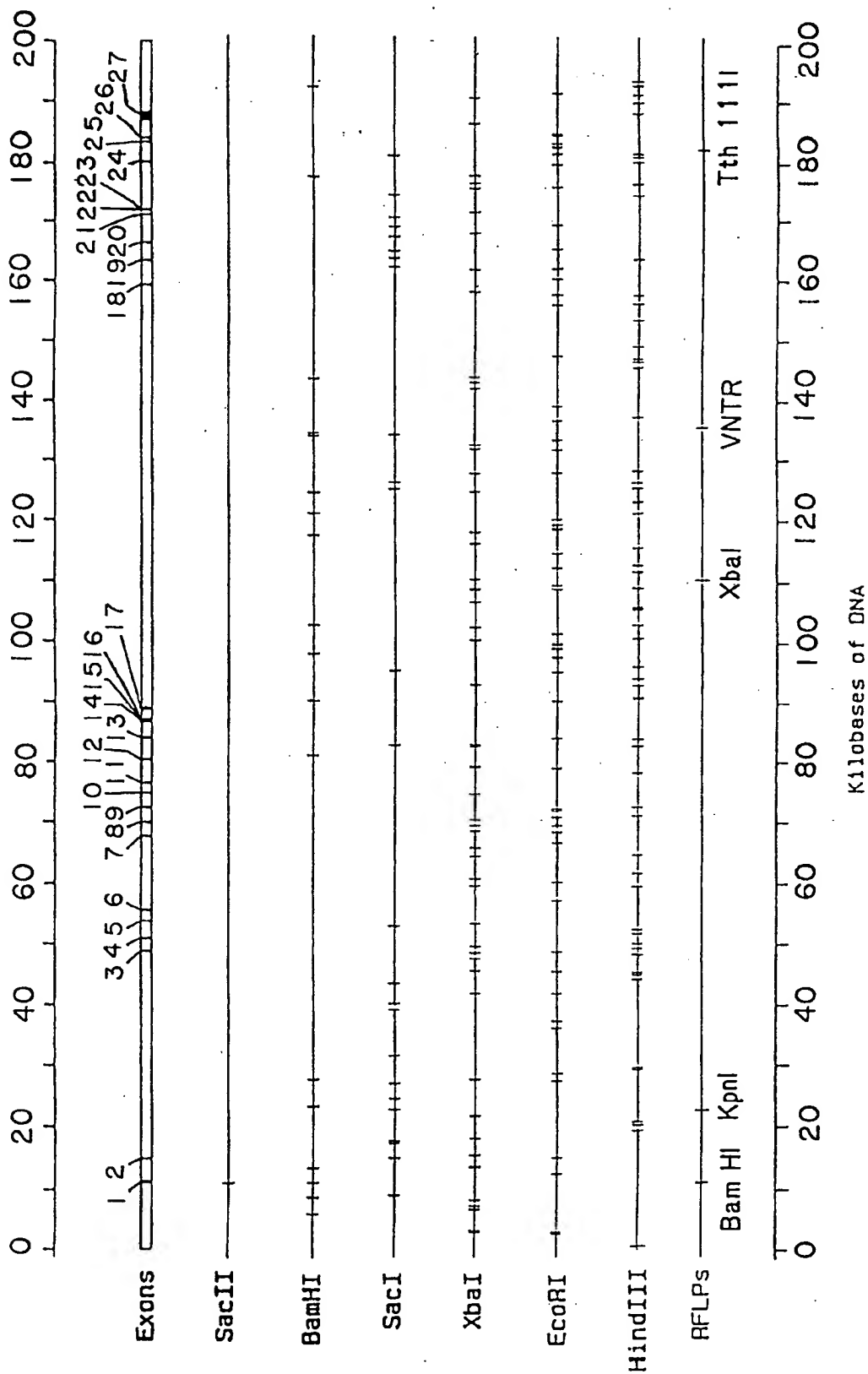


FIG. 5-1

GTCATGCCGCCCAAACCCCCGAAAAACGGCCGCCACCGCCGCGCTGCCGCCGCGGAACCCCCGGCACCGGCCGCCGC... 80
CCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAG... 160
AACCTGATTTTACTGCATTATGTCAGAAATTAAGATACCGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA... 240
GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAGAAAAAGAACTGTGGGAATCTGTATCTTTATTGCAGC... 320
AGTTGACCTAGATGAG..... 336

337	ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	378
	M S F T F T E L Q K N I E I	
379	AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC	420
	S V H K F F N L L K E I D T	
421	AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG	462
	S T K V D N A H S R L L K K	
463	TAT GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA	504
	Y D V L F A L F S K L E R T	
505	TGT GAA CTT ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT	546
	C E L I Y L T Q P S S S I S	
547	ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG ATC	588
	T E I N S A L V L K V S W I	
589	ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT	630
	T F L L A K G E V L Q M E D	
631	GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC	672
	D L V I S F Q L H L C V L D	
673	TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	714
	Y F I K L S P P M L L K E P	
715	TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA	756
	Y K T A V I P I N G S P R T	
757	CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA	798
	P R R G Q N R S A R I A K Q	
799	CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA	840
	L E N D T R I I E V L C K E	
841	CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA	882
	H E C N I D E V K N V Y F K	
883	AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT	924
	N F I P F M N S L G L V T S	
925	AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA	966
	N G L P E V E N L S K R Y E	
967	GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT	1008
	E I Y L K N K D L D A R L F	
1009	TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	1050
	L D H D K T L Q T S I D S	

FIG. 5-2

1051	TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA F E T Q R T P R K S N L O E	1092
1093	GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT E V N V I P P H T P V R T V	1134
1135	ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA M N T I Q Q L H M I L N S A	1176
1177	AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC S D Q P S E N L I S Y F N N	1218
1219	TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG C T V N P K E S I L K R V K	1260
1261	GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG D I G Y I F K E K F A K A V	1302
1303	GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT G Q G C V E I G S Q R Y K L	1344
1345	GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA G V R L Y Y R V M E S M L K	1386
1387	TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT S E E E R L S I Q N F S K L	1428
1429	CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT L N D N I F H M S L L A C A	1470
1471	CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG L E V V M A T Y S R S T S Q	1512
1513	AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG N L D S G T O L S F P W I L	1554
1555	AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC N V L N L K A F D F Y K V I	1596
1597	GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG E S F I K A E G N L T R E M	1638
1639	ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC I K H L E R L E H R I M E S	1680
1681	CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA L A W L S D S P L F O L I K	1722
1723	CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT Q S K D R E G P T D H L E S	1764
1765	GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA A C P L N L P L Q N N H T A	1806
1807	GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA A D M Y L S P V R S P K K K	1848

FIG. 5-3

1849	GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA	1890
	G S T T R V N S T A N A E T	
1891	CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT	1932
	Q A T S A F Q T Q K P L K S	
1933	ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC	1974
	T S L S L F Y K K V Y R L A	
1975	TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG	2016
	Y L R L N T L C E R L L S E	
2017	CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2058
	H P E L E H I I W T L F Q H	
2059	ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG	2100
	T L Q N E Y E L M R D R H L	
2101	GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG	2142
	D Q I M M C S H Y G I C K V	
2143	AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC	2184
	K N I D L K F K I I V T A Y	
2185	AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT	2226
	K D L P H A V Q E T F K R V	
2227	TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT	2268
	L I K E E E Y D S I I V F Y	
2269	AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG	2310
	N S V F H Q R L K T N I L Q	
2311	TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC	2352
	Y A S T R P P T L S P I P H	
2353	ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2394
	I P R S P Y K F P S S P L R	
2395	ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA	2436
	I P G G N I Y I S P L K S P	
2437	TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT	2478
	Y K I S E G L P T P T K H T	
2479	CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG	2520
	P R S R I L V S I G E S F G	
2521	ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC	2562
	T S E K F Q K I N Q H V C N	
2563	AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT	2604
	S D R V L K R S A E G S N P	

FIG. 5-4

2605	CCT AAA CCA CTG AAA AAA CTA CGC TTT CAT ATT GAA GGA TCA	2646
	P K P L K K L R F D I E G S	
2647	GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA	2688
	D E A D G S K H L P G E S K	
2689	TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA	2730
	F Q Q K L A E M T S T R T R	
2731	ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC	2772
	H Q K Q K M N D S H D T S N	
2773	AAG GAA GAG AAA	2784
	K E E K	

TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCAATTGTCTCTCACAGATGTGACTGTATAACTTTCC	2864
CAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGA	2944
YTCCTAAGCCACTTGAAATGTAGTCATTGTTATTTATACAAGATTGAAAACTTGTGTAAATCCTGCCATTTAAAAAGT	3024
TGTAGCAGATTGTTTCTCTTCCAAAGTAAAATTGCTGTGCTTTATGGATAGTAAGAATGGCCCTAGAGTGGGAGTCCTG	3104
ATAACCCAGGCCTGTCTGACTACTTTGCCTTCTTTGTAGCATATAGGTGATGTTTGTCTTTGTTTTATTAATTTATAT	3184
GTATATTTTTTAAATTTAACATGAACACCCTTAGAAAAATGTGTCTATCTATCTTCCAAATGCAATTTGATTGACTGCC	3264
ATTACCAAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAAAAAAATTAATAATTTACACATT	3344
AGATTTTATTTTACTATTGGAATCTGATATACTGTGTGCTTGTTTTATAAAATTTTGTCTTTAATTAATAAAAGCTGGA	3424
AGCAAAGTATAACCATATGATACTATCATACTACTGAAACAGATTTTCATACCTCAGAATGTAAAAGAACTTACTGATTAT	3504
TTTCTTCATCCAACCTTATGTTTTTAAATGAGGATTATTGATAGTACTCTTGGTTTTTATACCATTAGATCACTGAATTT	3584
ATAAAGTACCCATCTAGTACTTGAAAAAGTAAAGTGTTCTGCCAGATCTTAGGTATAGAGGACCCTAACACAGTATATCC	3664
CAAGTGCACCTTCTAATGTTTCTGGGTCTGAAGAATTAAGATACAAATTAATTTTACTCCATAAACAGACTGTTAATTA	3744
TAGGAGCCTTAATTTTTTTTTCATAGAGATTTGTCTAATTGCATCTCAAAATTAATCTGCCCTCCTTAATTTGGGAAGGT	3824
TTGTGTTTTCTCTGGAATGGTACATGTCTTCCATGTATCTTTGAACTGGCAATTGTCTATTTATCTTTATTTTTTTAA	3904
GTCAGTATGGTCTAACACTGGCATGTTCAAAGCCACATTATTTCTAGTCCAAAATTACAAGTAATCAAGGGTCATTATGG	3984
GTTAGGCATTAATGTTTCTATCTGATTTTGTGCAAAAGCTTCAAATTAACAGCTGCATTAGAAAAAGAGGCGCTTCTC	4064
CCCTCCCCTACACCTAAAGGTGATTTTAACTATCTTGTGTGATTAACCTATTTAGAGATGCTGTAACCTAAAAATAGGGG	4144
ATATTTAAGGTAGCTTCAGCTAGCTTTTAGGAAAAATCACTTTGTCTAACTCAGAATTATTTTTAAAAAGAAATCTGGTCT	4224
TGTTAGAAAAACAAAATTTTATTTTGTGCTCATTTAAGTTTCAAACCTACTATTTTGACAGTTATTTTGATAACAATGACA	4304
CTAGAAAACTTGACTCCATTTTCATCATTGTTTCTGCATGAATATCATACAAATCAGTTAGTTTTTAGGTCAAGGGCTTAC	4384
TATTTCTGGGTCTTTTGTCTACTAAGTTTACATTAGAATTAGTGCCAGAAATTTAGGAACTTCAGAGATCGTGATTGAGA	4464
TTTCTTAAATAATGCTTCAGATATTATTGCTTTATTGCTTTTTGTATTGGTTAAAACGTACATTTAAAATTTGCTATGT	4544
TACTATTTTCTACAATTAATAGTTTGTCTATTTTAAAAATAAATTAGTTGTTAG.....	4597

FIG. 6-1

	aaggagggag agtggngtcc ngngaggggt gcactagcca gatattctgc ggggccccgag	060
	agtcttccct atcagacccc gggataggga tgaggCCCAC AGTCACCCAC CAGACTCTTT	120
	GTATAGCCCC GTTAAGTGCA CCCCggcCTG GAGGGGTGG TTCTGGGTAG AAGCACGTCC	180
	GGGCGCGGCC GGATGCCTCC TGAAGGGCG CTGGACCCAC GCCAGGTTTC CCAGTTTAAT	240
	TCCTCATGAC TTAGNGTCCC AGCCNGCGCA CCGACCAGCG CCCCAGTTCC CCACAGACCG	300
<u>SacII</u>	CGGCGNGNNC GGGAGCCTGC GGACGTGAGC GCGGGCGGAA GTGACGTTTT CCGCGGTTGG	360
EXON 1	ACGCGGCGCT CAGTTGCCGG GCGGGGAGG GCGCGTCCGG TTTTCTCAG GGGACGTTGA	420
	start of cDNA sequence	
	AATTATTTTT GTAACGGGAG TCGGGAGAGG ACGGGGCGTG CCCCgCGTGC GCGCGGTCG	480
	TCCTCCCCGG CGCTCCTCCA CAGCTCGCTG GCTCCCGCG CCGAAAGGCG TCATGCCGCC	540
	MetProPr	(3)
<u>SacII</u>	CAAAACCCCC CGAAAAACGG CCGCCACCGC GCGCGTGC CCGCGGAAC CCCCgCACC	600
	oLysThrPro ArgLysThrA laAlaThrAl aAlaAlaAla AlaAlaGluP roProAlaPr	(23)
	GCCGCGCGCG CCCCCTCCTG AGGAGGACCC AGAGCAGGAC AGCGGCCCCG AGGACCTGCC	660
	oProProPro ProProProG luGluAspPr oGluGlnAsp SerGlyProG luAspLeuPr	(43)
	TCTCGTCAGG TGAGCGAGCA GAGCGCGTCN CTCACGCGGG AAGGGCGCCC CGGGTGTGCG	720
	oLeuValAr	(46)
	TAGGGCGGGC GCAAGGCGgC TCGGGGGGA CCCGTCCTCG CCAGGGgCCG GGTCCgGNG	780
	GGAGGAGGCG CCCTCCCTGC CCCCgGCCAC GGcggaGCGT CTGCAGAATG GTGACAGGAT	840
	TCTGGGTTCT TGGGCGAGGG GTCTCGGCTT CAACTTGACA GGTGTCGGGC GGGTggggct	900
	agnntcctga gcgaagtgc aggtgcagtt ccctcttctg agnctcgan ncagaggntc	960
	gttcgagcg tncatcagac aaaaaaatga aaataaaaa taacaaaa	1008
	--2.9 kb--	
	cccaaacagc tttagctatt acatttactt tccttcacag aagtgttttg ctgctttgaa	060
	gatatttgac ttaccatgca agcaaatatt tttcactgtg tggatccctt attttggaat	120
	gaccatgaaa aagataatca tatgnnnaaa tttgaagtgt aatgtttttc taagataaaa	180
	taagatcttA AAGTATTIAA TAATGTTCTT TTCACAGTA GTGTTATGTG CAAACTATTG	240
	AAACAAGTAT GACTGAATC AATTTGATTI ATAAGATATG CCAATTATAT GATTATTTTC	300
EXON 2	ATTTGGTAGG CTTGAGTTTG AAGAAACAGA AGAACCTGAT TTTACTGCAT TATGTCAGAA	360
	g LeuGluPheG luGluThrGl uGluProAsp PheActAlaL euCysGlnLy	(63)
	ATTAAAGATA CCAGATCATG TCAGAGAGAG AGCTTGGTTA ACTTGGGAGA AAGTTTCATC	420
	sLeuLysIle ProAspHisV alArgGluAr gAlaTrpLeu ThrTrpGluL ysValSerSe	(83)
	TGTGGATGGA GTATTGGTAA GGATTTTCTT AAAACGTTTT GAAATTTTTT TTTCTCATTT	480
	rValAspGly ValLeu	(88)
	TAAAACCAAC TTCAAATCAC TATACAAAA TTGAAAGATA GAAAAATATA AAGACAATAA	540
	AAGctaataa taattccatt acccagagga aatttacctc tgctaacatt aaaaatgttt	600
	gaggccgggc acgtgggttc tgccgtgaat cctaccactt tgggaggctg aggcaggtgg	660
<u>SacI</u>	attgcctgag ctcaggagtt cgagaccagc ctgggcaaca tgggt	704
	--33 kb--	
	ctattttgaga tgactgacce ctaaaagtcc acaataacta ttttaattttt tatctttcta	060
	atactttttt gccttataat ataaaatttg aatgtttgtt attagtgtga aatgaaatcc	120
	tttcaaatat atgccatcag aaggatgtgt tacaaatata cagtATTACA AACATTTATT	180
	TTGTATGCTG AATAAGAAAA AATCAGTTAT AATACAGTTT TAACATAGTA TCCAGTGTGT	240
EXON 3	GAATTATTTA ATGAAATATT TGATCTTTAT TTTTGTTC AGGGAGGTTA TATTCAAAAG	300
	GlyGlyTy rIleGlnLys	(94)
	AAAAAGGAAC TGTGGGAAT CTGTATCTTT ATTGCAGCAG TTGACCTAGA TGAGATGTCTG	360
	LysLysGluL euTrpGlyIl eCysIlePhe IleAlaAlaV alAspLeuAs pGluMetSer	(114)
	TTCATTTTTC CTGAGCTACA GAAAAACATA GAAATCAGGT AAAGTTTCTT GTATAAATAT	420
	PheThrPheT hrGluLeuGl nLysAsnIle GluIleSe	(127)
<u>EcoRI</u>	AAGCCTCTGC CATAAAAGGA AACGAATCTT GGATTTTCCT CTCAATAGAC TTTTGTGAAT	480
	TAGTGAGAAA TGCTAAAATA AAGTAAAACA AAAAGAACTT GGACCAAATA GTGAAGTCCC	540
	ATTCTCTCAT GGAGCCGTTA TGAAGTGTA TTTATGCTGT ATTTCTTTAA GAGGTAGCAG	600
	TTGTGTCTCT GGAAAAATTT TCATTGTGTC TCTCACTATT CATGTGTAAG C	651
	--1.6 kb--	

FIG. 6-2

	gcataggtat	atagataata	gaggtgtaag	ttgaaggcra	attatTTTTg	caaaaagtaa	060
	ttccttccaa	aggatatagt	agtgatttga	tgtagagctg	ataatcTTTT	GAATTGAAAT	120
	ATCTATGATT	TGAAAACGAA	ATAACACAAA	TTTTTAAGGT	TACTGATTTA	CTTTTTTCTA	180
EXON 4	TTCTTTTCCTT	TGTAGTGTCC	ATAAATTCTT	TAACCTTACTA	AAAGAAATTG	ATACCACTAC	240
		rValH	isLysPhePh	eAsnLeuLeu	LysGluIleA	spThrSerTh	(142)
	CAAAGTTGAT	AATGCTATGT	CAAGACTGTT	GAAGAAAGTAT	GATGTATTGT	TTGCACTCTT	300
	rLysValAsp	AsnAlaMetS	erArgLeuLe	uLysLysTyr	AspValLeuP	heAlaLeuPh	(162)
	CAGCAAATTG	GAAAGGTAAA	GTAACACATT	TATTAGGGTT	ACACTCTGAT	TTTTTATGTC	360
	eSerLysLeu	GluAr					(167)
	ATTGTTTACA	ATTAGATTCT	GGGAATTATT	TAACACATT	AGTAAAGTTA	GTAAGTATTA	420
	ATTCTTAGac	ttgtcccttt	taatgttagc	tcattaattc	ttagctttct	tatttatcca	480
	gtaatatgca	ttctgaatgc	ttcctggaaa	attaaccgtt	attatccctt	catgtctcca	540
	tttgttttca	aaacttagct	tatcgagtat				570
	--2.1 kb--						
	gagatattta	aagagnaact	ttactaacct	tagtgggac	agctgggtgt	tttctatctt	060
	atttatacct	tttttttgaa	GACTAATTGA	GAGGATTAAAC	TGTAATTATA	TATTAAAGTG	120
	ATGTGAGATG	TCATAAATTG	GGAAAATCTA	CTTGAACCTT	GTTTTATAAT	GCTATATATT	180
	TTTTGTTTTT	AAAATATATA	CTTCTTAAAA	GAAGATGAAT	AAAGCATGAG	AAAACACTA	240
EXON 5	TGACTTCTAA	ATTACGAAAA	AATGTTAAAA	AGTCATAATG	TTTTTCTTTT	CAGGACATGT	300
					gThrCys		(169)
	GAACCTATAT	ATTTGACACA	ACCCAGCAGT	TCGTAAGTAG	TTCACAGAAT	GTTATTTTTTC	360
	GluLeuIleT	yrLeuThrGl	nProSerSer	Se			(180)
	ACTTAAAAAA	AAAGATTTTT	ATGGAATAAT	CTCAAACATC	TTGATAGTTA	GGGTTAGTTT	420
	GATCGATTAT	AGCAGGCTAC	Ttcataaatt	aagcccatag	atttaagtc	tgtgtagatt	480
	atttatcttc	tcacaaagaa	aatagtataa	aatacatgcc	ttgtactaca	sagaagaact	540
	aataaggtgg	aattgattca	ggacagcata	tcaccaactc	tgagaaaaat	gcaacaaatg	600
	caaattcatt	gactaa					616
	--1.4 kb--						
	aatggactg	cattctatta	tgcatttaac	taaggtcatt	ttttttttta	tGCACAAAAA	060
	GAAACACCCA	AAAGATATAT	CTGGAATAAT	TTCTTTTCACT	GATACATTTT	TCCTGTTTTT	120
EXON 6	TTTCTGCTTT	CTATTTGTTT	AATAGGAAAT	CTACTGAAAT	AAATTCTGCA	TTGGTGCTAA	180
			rIleS	erThrGluIl	eAsnSerAla	LeuValLeuL	(192)
	AAGTTTCTTG	GATCACATTT	TTATTAGCTA	AAGGTAAGTT	CATTATATTT	ATTAATGCT	240
	ysValSerTr	pIleThrPhe	LeuLeuAlaL	ysG			(203)
	AATATTTCAA	ATGTAATAAT	TAAATTGGCA	TTCTTTTGA	CTAAATTCCT	CAATTTTTAT	300
	TGAGTAATGT	ACTCCTccct	cattctctgc	ttggcttatt	aactgttagc	aagttccctat	360
	aattctggta	ctagaaacaa	ccttggaat	gctttattta	atntttgttt	ctaattatcc	420
	atcttccctc	cctt					434
	--11.5 kb--						
	tttatagtga	ttttagacat	aaagaattaa	ttataacaga	aatagcttaa	atgtaaaatt	060
	ctcagagtag	agcttaacac	ttgatttata	attccataac	tttacatatt	tCTATTTTAC	120
	ATATTTTATA	CGTTTTAAAA	CAGATTTTTT	TTTTTTTTTAC	AAAAAAAAGA	AAGAAAATCT	180
	TTACCATGCT	GATAGTGATT	GTTGAATGAA	TAAATTTATG	GATATACTCT	ACCGTGGCAT	240
	TTTCTCTCAT	ACAAAGATCT	GAATCTCTAA	CTTCTTTTAA	AAATGTACAT	TTTTTTTTCA	300
EXON 7	GGGGAAGTAT	TACAAATGGA	AGATGATCTG	GTGATTTCAT	TTCAGTTAAT	GCTATGTGTC	360
	lyGluValL	euGlnMetGl	uAspAspLeu	ValIleSerP	heGlnLeuMe	tLeuCysVal	(222)
	CTTGACTATT	TTATTAAACT	CTCACCTCCC	ATGTTGCTCA	AAGAACCATA	TAGTAAGTAT	420
	LeuAspTyrP	heIleLysLa	uSerProPro	MetLeuLeuL	ysGluProTy	rL	(240)
	TTAATTTATG	CCCCTTTTAC	TTTCTCATT	AGCAGTTGCT	TATTGAATGT	CTAGTGGGTA	480
	CCAAACATGG	TTCTAAGGCT	GACAGGATGA	TAAAAAATAA	ATCAgacatg	gactttgccc	540
	ataagtagtg	taagttatag	aaggaaagat	aagacatgga	aacaaatgat	tagagtatat	600
	ggtagaaagt	ggtttcgggt	caaaatacaa	caaatggagg	tttgggagac	aagaag	656
	--1.8 kb--						

FIG. 6-3

	gctattccat	gccttctctt	tgtatttgtt	tatgagactg	tagttttacg	ttcttttttgg	060
	gannagagta	gaagagggat	gCAAAAACCTA	ATATTAGTAC	ATAATTTGTA	GTAGATATGC	120
	ATGAAATTGT	TATCCTTCTA	ATGAAACCTA	ATAAGTAAAA	CTAGTAGAAT	GTTACCAAGA	180
	TTATTTTTGA	CCTAAGTTAT	AGTTAGAATA	CTTCATTATT	TTATATGATG	GATGTACAAT	240
EXON 8	TGTTCTTATC	TAATTTACCA	CTTTTACAGA	AACAGCTGTT	ATACCCATTA	ATGGTTCACC	300
			y	sThrAlaVal	IleProIleA	snGlySerPr	(250)
	TCGAACACCC	AGGCGAGGTC	AGAACAGGAG	TGCACGGATA	GCAAAACAAC	TAGAAAATGA	360
	oArgThrPro	ArgArgGlyG	lnAsnArgSe	rAlaArgIle	AlaLysGlnL	euGluAsnAs	(270)
	TACAAGAATT	ATTGAAGTTC	TCTGTAAAGA	ACATGAATGT	AATATAGATG	AGGTAATTTA	420
	pThrArgIle	IleGluValL	euCysLysGl	uHisGluCys	AsnIleAspG	lu	(287)
	ACTTCATGAT	TTCTTTAAAA	CAGTTAAAGT	AGATTTAGAT	GTAAGTTCTC	CCTAACAAATA	480
	TTTACTTCTT	TTGTTATGAG	CATGTTTTTT	TTGTAATTAG	TGCTAACTCT	TTTGCAGTAG	540
	CAAAATATTT	AGAAAAAtta	attcggtata	tttagttact	ttgattttaag	agagtagctc	600
	cctcactct						609
				--1.8 kb--			
	aagcattgas	gctgtaatgc	atgtgattgc	acctgtgaat	agccactaca	cttcagccta	060
	ggcaatatag	agagaccctt	tctcTAAGAA	AATAATAAAA	AATAAAAAAG	TTATACACAG	120
	ATTTTTTACT	GCATGGGGGA	TTGACACCTC	TAACTTACCC	TGCATTGTTT	AAGAGTCAAG	180
EXON 9	AGATTAGATT	TTGTITTAAT	TTTTAATGAT	CATGTTGTAA	CTTCATCTTT	TTCAGGTGAA	240
					VallY		(289)
<u>EcoRI</u>	AAATGTTTAT	TTCAAAAATT	TTATACCTTT	TATGAATTCT	CTTGGACTTG	TAACATCTAA	300
	sAsnValTyr	PheLysAsnP	heIleProPh	eMetAsnSer	LeuGlyLeuV	alThrSerAs	(309)
	TGGACTTCCA	GAGGTAATCT	GAAAGGAAAT	TTAATAAAAT	ATTAATGTTT	TGAGACTGTG	360
	nGlyLeuPro	Glu					(313)
	GAGGGAGGAT	AATTGTCTAA	CTTCTTAGA	TCAATTTACT	GTGTATCACA	TTTTTTTTTT	420
	CCCCAAGAAG	AATCTAGCCA	AGTAGAATTG	TGGTGAAACT	AACTTTTGTA	TAGTAacaaa	480
<u>HindIII</u>	aagctt						486
				--1.9 kb--			
	gtagcattgg	ctatctttgt	ctacataaaa	ttctaataaa	tattttctat	gcacgAAATA	060
	GACCTAAAT	CAAAGTTGAA	CAAATGTTGC	AATTTTCTGT	ACCTCACTTT	TAGATAGACC	120
	TTATTTTAT	TGCATGCGAA	CTCAGTGTAT	ATTACAAAAT	TAAATGTATA	TTATACAAAA	180
	ATTCTTTAAT	GAAATCTGTG	CCTCTGTGTG	CTGAGAGATG	TAATGACATG	TAAAGGATAA	240
EXON 10	TTGTCAGTGA	CTTTTTTCTT	TCAAGGTTGA	AAATCTTTCT	AAACGATACG	AAGAAATTTA	300
			ValG1	uAsnLeuSer	LysArgTyrG	luGluIleTy	(325)
<u>XbaI</u>	TCTTAAAAAT	AAAGATCTAG	ATGCAAGATT	ATTTTGGAT	CATGATAAAA	CTCTTCAGAC	360
	rLeuLysAsn	LysAspLeuA	spAlaArgLe	uPheLeuAsp	HisAspLysT	hrLeuGlnTh	(345)
	TGATTCTATA	GACAGGTATT	GCACATGGTA	TATTTGATTG	ATTTGCTTTA	GATATAGGTT	420
	rAspSerIle	AspSe					(350)
	GATACTGATA	TAGGTAGATT	ATATAGTCTT	TAGCTTAGTG	ACCTTTAGAT	ATCATTTATA	480
	ACAAATTACT	TTCAAATGTC	TTTATACAAA	GAAAAGTTTA	ACAGTATTTT	AAGcatataa	540
	cttatctaca	aatatagatt	taatgtgaat	tgtgtgtcct	ataacagtta	ccttttttnc	600
	gttaactgaa	tataattttt	aaaatgtgca	ccaaaagata	atggcta		647
				--1.0 kb--			

FIG. 6-4

	aataactgaac	aacttggtta	tcaataaccnc	cagggagaag	catctgactt	tcacttttaa	060
	aaaaagactt	aatgattggt	atacctcttt	gtcataaaca	taatggaaag	agaccacaaa	120
	ttaaaaagng	tagtgAAAGG	TATTTTATTT	AAGCAGCAGC	TGGGTCATCT	ATTTTCTATC	180
	CTATCTATTA	TTGAGTTATC	ATTTTATATG	ATTTTATGAG	ACAACAGAAG	CATTATACTG	240
	CTTTTTTGAT	GCATAAAGCA	CAAATTGTAA	ATTTTCAGTA	TGTGAATGAC	TTCACTTATT	300
EXON 11	GTTATTTAGT	TTTGAACAC	AGAGAACACC	ACGAAAAAGT	AACCTTGATG	AAGAGGTGAA	360
		r PheGluThrG	lnArgThrPr	oArgLysSer	AsnLeuAspG	luGluValAs	(367)
	TGTAATTCCT	CCACACACTC	CAGTTAGGTA	TGAATTTTCC	TACTTTTAAT	TATATTATAA	420
	nValIlePro	ProHisThrP	roValAr				(326)
	TTTTGTATT	CATGGCTTTA	TAGTGTTC	GATTGTTC	CGTTTCTTTA	TGTATTCATA	480
	CATACATGTA	AGAAATATAT	ATTGAAGGCC	AGGTGTGGTG	GATCACACCT	GTAATCCAG	540
	CACTTTGGGA	GGCCAAGGCG	GGCAGATCAC	CTGAGGTTAG	GAGTTTGaga	ccggcctggc	600
	caacatgggtg	aaaccccgte	tctactagaa	atacaaaaat	tagctg888g	t8gt8gt8t8	660
	tgcctgtaat	ccagctgctc					680
	--3.2 kb--						
	caataccatt	ttgttgccag	ttatatagtt	ctcctaaaaa	taatgccACT	ATTTTATTGA	060
	TATGTAGTTT	TATTAGTAAA	TAAGTATATC	TGTTCTATAA	CTATAAACTT	ATTGATTGTG	120
	AATACATATT	TTCTTAAAGA	TTTAAAGTAA	ATGTAATTTC	TTATAAACCA	CAGTCTTATT	180
	TGAGGGAATG	TAGAGACAAG	TGGGAGGCAG	TGTATTTGAA	GATACATTTA	ACTTGGGAGA	240
	TTGAAAACAT	TTCAATTTTT	CTTTTTTCT	CCCTTCATTG	CTTAACACAT	TTTCCTATTT	300
EXON 12	TTATCCCTC	TAGGACTGTT	ATGAACACTA	TCCAACAATT	AATGATGATT	TTAAATTCAG	360
		gThrVal	MetAsnThrI	leGlnGlnLe	uMetMetIle	LeuAsnSerA	(392)
	CAAGTGATCA	ACCTTCAGAA	AATCTGATTT	CCTATTTTAA	CGTAAGCCAT	ATATGAAACA	420
	laSerAspG1	nProSerGlu	AsnLeuIleS	erTyrPheAs	n		(405)
	TTATTTATTG	TAATATCTTG	GCAAAGAAAC	TTGAAATTAA	AAGTTAAAGT	ACTGAGTTCT	480
	TTTTAAATA	CTAATCTCCT	ATCTAACATG	TAGTTATCCA	TAATCTTTTC	TTGCTTTTTT	540
	AATCTTACAA	ATTATATATT	ATTAGTAGTA	TTGTTTTTATT	TATACAGTGT	TATTTAAAC	600
	ATTTTATGT	TTACCTATTT	GCCTTgetca	ccattcttcc	ttcgaactta	tgcctcactt	660
	ctgagataat	tttttcttct	tcagatatat	cctttgataa	ttac		704
	--3.1 kb--						
	aaaatttaga	taatagggtt	ttttagttgt	actgtagtat	tttttgetcg	attaacatcc	060
	AGTGAATGA	TATTGCTGCG	TTATGTTTCT	TAGTTGTGGT	TACCTAGTTA	TTATGGAAGT	120
	GTTTCCACAT	TTTTATGAAC	AATTTAAAAA	GTCATATATT	ATGGAGCAGA	AAATATTAAT	180
EXON 13	TCTGATTACA	CAGTATCCTC	GACATTGATT	TCTGTTTTTA	CCTCCTAAAG	AACTGCACAG	240
						AsnCysThrV	(409)
	TGAATCCAAA	AGAAAGTATA	CTGAAAAGAG	TGAAGGATAT	AGGATACATC	TTTAAAGAGA	300
	alAsnProLy	sGluSerIle	LeuLysArgV	allLysAspIl	eGlyTyrIle	PheLysGluL	(429)
EcoRI	AATTIGCTAA	AGCTGTGGGA	CAGGGTTGTG	TCGAAATTGG	ATCACAGGTA	ACTTGAATTC	360
	ysPheAlaLy	sAlaValGly	GlnGlyCysV	alGluIleG1	ySerGln		(444)
	ATTGTAAATC	GTGGTACTAT	AGAGTAATAA	TATTAAGAGC	AGCATCTTTC	CAGTTCGTAT	420
	AAATACTCTA	ACAGTATTTG	TCTAGTAGTA	TAAAATACTG	TCAGATACTA	TATCCCTGCT	480
	GCCTGTGTAT	GCTGCTATTT	ATGGGAACCT	TATGGAAAAC	TACCTCCCAc	cccattataa	540
	aaactatgta	ataaaggaac	acatagccat	tgtagaaatt	ttng		584
	--1.8 kb--						

FIG. 6-5

	gaatgttaaat	caccacttaa	tacttaagtt	gtgagtttta	gacaagctng	cttttgtgtt	060
	gtcttggcgg	ccatatttgt	aagaagggtg	AGAAGTATGT	TTTAAGAAAA	GGCTTTTTAA	120
	AAAATTTTAG	TAATTGTCAG	CTGGGTATAG	TGGTACATGC	CTATAATCCC	AGCCTCTTGG	180
	GAGGCCAAAG	CAGGAGGATC	TCTTGAGCCC	AGGAGTGTGA	AGGCCAGCCT	GGGCAAAACA	240
	GTGAGACTCC	ATCTCAAAAA	AAAAAAAAAA	TTTCATAATT	GTGATTTTCT	AAAATAGCAG	300
EXON 14	GCTCTTATTT	TTCTTTTTGT	TTGTTTGTAG	CGATACAAAC	TTGGAGTTCG	CTTGATTATC	360
				ArgTyrLysL	euGlyValAr	gLeuTyrTyr	(454)
	CGAGTAATGG	AATCCATGCT	TAAATCAGTA	AGTTAAAAAC	AATAATAAAA	AAATTTTCANC	420
	ArgValMetC	luSerMatLe	uLysSer				(463)
	CGGGCGCGGT	GGCTCACGCC	TGCAATCCCA	GCACTTTGGG	AGGCCGAGGT	GGGCAGATCA	480
	GGAGGTCAG	GCATCAAGAT	CATCCTGGCC	AAAATGGTGA	AACCCTGTCT	CTACTAAAAG	540
	TACAAAAATT	AGCTGGGCGT	GGTGGTGTAG	ACCTGTAGTC	CCAGCTACTT	GGCAGGCTCA	600
	GGCAGGAGAA	TCCCTTGAAC	CACGGAGGTT	GAGGTTGCAG	TGAGCCAAGA	TTGTGCCATT	660
	TCACCCACAG	CTGGCAACAG	AGCAAGACAC	CATCTAAAAA	AAAAAAAAAA	AAAAAAAAAA	720
	ATTCAATGCT	GACCAAAATA	AGGTTTCAAT	TAAACAACTT	CTTTTTTTTT	TTTTAAATTA	780
EXON 15	TCTGTTTCAG	GAAGAAGAAC	GATTATCCAT	TCAAAATTTT	AGGTAATTTT	TTTACTTTTA	840
		GluGluGluA	rgLeuSerIl	eGlnAsnPhe	Se		(474)
	GTAAAAAATT	TTTTTCTTTT	TATAGAAGTA	AGTATTTTAT	AATCTTTTTT	TTTTTCCTTT	900
EXON 16	AGCAAACCTC	TGAATGACAA	CATTTTTCAT	ATGTCTTTAT	TGGCGTGGCG	TCTTGAGGTT	960
	rLysLeuL	euAsnAspAs	nIlePheHis	MetSerLeuL	euAlaCysAl	aLeuGluVal	(493)
	GTAATGGCCA	CATATAGCAG	TAAGTTAAAT	TTTCATAAAT	AAACACTTTT	GTTCAATTTA	1020
	ValMetAlaT	hrTyrSerA					(500)
	AAGTTAAAAAT	GTGGTGTGTT	TCTTTGGTCT	GGGGAGAGGG	ATAGTGTGAG	GTTAAGGAGA	1080
	AGGAATGCTT	ATTTTAGATC	ACTATATACT	GAAGAATGTA	ATTGGTCAAT	ATAAGCCATT	1140
	TAAGAGGCTT	ATTTGAGTTA	TTTGAggcca	tcttggggat	aatattttcac	taggctttctc	1200
	ttctzagtat	actggtatac	tgaatccaaa	aaaggtactt	tttcgaaatc	cctccgaaga	1260
	cctttzagat	tgtagagtgc					1280
			--1.0 kb--				
	ggtattttaa	tctttgaaaa	tttgagatca	gctataagtc	ctttctctag	gaaaaacaca	060
	gaTTTGCATA	CACTCAAAAT	TGGAAGGCTA	TTTCCTATGA	GTCCGTAGAC	TCCAAAATAA	120
	AAAATTCTGC	TCTAAATAAA	AATGGTTTAA	CCTTTCTACT	GTTTTCTTTG	TCTGATAATA	180
	ACTTCCAAAA	AAATACCTAG	CTCAAGGGTT	AATATTTTCAT	AAATAGTTAC	TTTTTTTTTT	240
EXON 17	CATTTTTIAGG	AAGTACATCT	CAGAATCTTG	ATTCTGGAAC	AGATTGTGCT	TTCCCATGGA	300
	r	gSerThrSer	GlnAsnLeuA	spSerGlyTh	rAspLeuSer	PheProTrpI	(517)
	TTCTGAATGT	GCTTAATTTA	AAAGCCTTTG	ATTTTACAA	AGTGATCGAA	AGTTTTATCA	360
	leLeuAsnVa	lLeuAsnLeu	LysAlaPheA	spPheTyrLy	sValIleGlu	SerPheIleL	(537)
	AAGCAGAAGG	CAACTTGACA	AGAGAAATGA	TAAAACATTT	AGAACGATGT	GAACATCGAA	420
	ysAlaGluGl	yAsnLeuThr	ArgGluMetI	leLysHisLe	uGluArgCys	GluHisArgI	(557)
	TCATGGAATC	CCTTGCAATG	CTCTCAGTAA	GTAGCTAAAT	AATTGAAGAA	ATTCATTCAT	480
	leMetGlySa	rLeuAlaTrp	LeuSer				(565)
	GTGCATATGG	CTAACAAATG	ATTGTTAGTG	AGAGGTGTTT	CTTAACAAAT	CTACCTCAAG	540
	AACAAATAGG	GAATTTAATG	AATAATGTTA	TTTCAGTCTA	TAGCCCAAGG	ATCAagtggga	600
	atattagaat	ggagcttttaa	tczagcacc	taaaccatct	aatacagcnc	agtgatcttat	660
	ttaagaatag	cttttctttaa	aacatgccac	ttt			693

-70.0 kb--

FIG. 6-6

	..cttctaataa	ataagcgttg	aagggtatac	atctttctac	ttttttgtgt	gtgggaagta	060
	caaaaattgt	CAATTGGGAA	TTTCGAAGTA	GAGAAAAATA	TTTCATTCTG	ACTTTTAAAT	120
	TGCCACTGTC	AATTGTGCCT	AAAATTCATA	GTACTTACCA	TGTCAAACAA	TATGATTTTG	180
EXON 18	ATATGTACCT	GGGAAAATTA	TGCTTACTAA	TGTGCTTTTA	ATTTTCATCAT	GTTTCATATA	240
	GGATTACCT	TTATTTGATC	TTATTAAACA	ATCAAAGGAC	CGAGAAGGAC	CAACTGATCA	300
	AspSerPro	LeuPheAspL	euIleLysG1	nSerLysAsp	ArgGluGlyP	roThrAspHi	(585)
	CCTTGAATCT	GCTTGTCTC	TTAATCTTCC	TCTCCAGAAT	AATCACACTG	CAGCAGATAT	360
	sLeuGluSer	AlaCysProL	euAsnLeuPr	oLeuGlnAsn	AsnHisThrA	laAlaAspMe	(605)
	GTAAGCAAAA	TATATGTTAT	GTTGACCATC	AAACTGCAAA	TAGATTTTAA	GCATAAGTGC	420
	AATGTAACAT	TCTATAAAGA	AAGTGTAGGG	AATAGAATTT	TGAATAAGAA	TAGTTTCTGT	480
	TTTTAAGAAA	TTAGTAATAA	AAGGTACATg	acccaaataa	agtcataataa	aagagtacag	540
	agtgcactctg	aatcacctag	gatttgcata	atgagagcag	ttttcatgg		589
	--3.0 kb--						
	tgtttttaag	ctggaatcac	cttatggctt	caataccact	ataattatta	aaattgTACA	060
	TTATACATAT	ATAGCTATTT	TTTTCTAATA	AGGCAGTAAT	CCCCAGGAAA	AGCCATTTAT	120
	TAAAATAGAA	TTAGATATGA	TGATGACAAG	CAGTTTTCCCT	ATTAATATAT	CTTTCCCAGC	180
	TTGCATTTAA	ATAGTCTGCT	ATAATACCAA	TTAAATAGAC	AAGATGTATC	TGGGTGTACA	240
	ACCTTGAAGT	GTATGTATAA	TCTGTGATTC	TTAGCCAACT	TGAAATGAAG	ACTTTTCCTT	300
EXON 19	TAAATATATC	TAGGTATCTT	TCTCCTGTAA	GATCTCCAAA	GAAAAAAGGT	TCAACTACGC	360
		tTyrLeu	SerProValA	rgSerP=OLy	sLysLysGly	SerThrThrA	(621)
	GTGTAAATTC	TACTGCAAAT	GCAGAGACAC	AAGCAACCTC	AGCCTTCCAG	ACCCAGAAGC	420
	rgValAsnSe	rThrAlaAsn	AlaGluThrG	lnAlaThrSe	rAlaPheGln	ThrGlnLysP	(641)
	CATTGAAATC	TACCTCTCTT	TCACTGTTTT	ATAAAAAAGG	TTAGTAGATG	ATTATTTTCA	480
	roLeuLysSe	rThrSerLeu	SerLeuPheT	yrLysLysV			(654)
	AGAGCATGGA	CTCTGAAACT	AGGCTGACTG	GTTTCAAATC	ATGTTTCTTC	TACTTTCTAG	540
	GTACATTACT	GGGCAAGTCA	CTTAATATCT	CTGTGTCTCA	GTTTCCTcat	ctataaaatg	600
	gaaatgataa	tgttzcgaga	tctttcttga	ctatttcagag	tcgttttctg		650
	--2.8 kb--						
	aaggaaaatc	catgccccnt	cgggacatgc	ctgncctctg	cattttctca	tctgtatccc	060
	ttgtaatatg	cctcataata	saccagtaaa	catGTTTCTC	TGGGGGAAAG	AAAAGAGTGG	120
	TAGAAAAGAG	GTTTCTGTTA	AAATGCTACT	TAACAGCATT	ATAATTAGTG	TAATTTTCATG	180
	ATTTGAAAAA	AATCTACTTG	TAATTCAAAA	TGAACAGTAA	AAATGACTAA	TTTTTCTTAT	240
EXON 20	TCCCACAGTG	TATCGGCTAG	CCTATCTCCG	GCTAAATACA	CTTTGTGAAC	GCCTTCTGTC	300
	al	TyrArgLeuA	laTyrLeuAr	gLeuAsnThr	LeuCysGluA	rgLeuLeuSe	(671)
	TGAGCACCCA	GAATTAGAAC	ATATCATCTG	GACCCTTTTT	CAGCACACCC	TGCAGAATGA	360
	rGluHisPro	GluLeuGluH	isIleIleTr	pThrLeuPhe	GlnHisThrL	euGlnAsnG1	(691)
	GTATGAACTC	ATGAGAGACA	GGCATTGGGA	CCAAGTAAGA	AAATCAAGCA	CTTCACCTTC	420
	uTyrGluLeu	MetArgAspA	rgHisLeuAs	pGln			(702)
	TCTCCTCCCT	ACTTACTTGT	TAAGTGATTT	CTTTCTTTCT	TTCTTTCTTT	CTTTCTTTCT	480
	TTCTTTCTTT	CTTTCTTTCT	TTCTTTCTTT	TCTTTTCTTT	CTTTCTTTCT	TTCTTTCTTT	540
	TTTTTTTGAG	ATAGAGTCTC	ACTCTGTTAC	CCAGGCTGGA	GTGCAGTGGC	GCAATCTCGG	600
	CTCACTGCAA	CCTCCGCCCT	CCAGGTCAAG	TGATTCTCCT	GCCTCAGCCT	ccnaggagct	660
	aggatacagg	cgtgtaccac	cacaccttgt	taatttttgt	tatttagtag	agacagg	717
	--4.0 kb--						

	caagagccaa	agttagggtg	atttacaac	caggtgatca	gtcctggata	attgagcctt	060
	ggtgatttgC	ATTTTGTTC	TAAACACAC	TTTGGGTAA	ACACTTCATG	TAGACTTTCA	120
<u>SacI</u>	AACTGAGCTC	AGTATGGAAA	GAAATAACTC	TGTAGATTAA	ACCTTTCTTT	TTTGAGGCTA	180
	AAAGAAAAGAA	AATGGTATTT	TTTAAGAACA	AAACCATGTA	ATAAAATTCT	GACTACTTTT	240
EXON 21	ACATCAATTT	ATTIAC TAGA	TTATGATGTG	TTCCATGTAT	GGCATATGCA	AAGTGAAGAA	300
		I leMatMetCy	sSerMetTyr	GlyIleCysL	ysValLysAs	(716)	
	TATAGACCTT	AAATTCAAAA	TCATTGTAA	AGCATACAAG	GATCTTCCTC	ATGCTGTTCA	360
	nIleAspLeu	LysPheLysI	leIleValTh	rAlaTyrLys	AspLeuProH	isAlaValGl	(736)
	GGAGGTAGGT	AATTTTCCAT	AGTAAGTTTT	TTTGATAAAT	CCATATCCAT	AACATAACAT	420
	nGlu						(737)
	AGGTAATTCA	TTTGATCTCA	TTTATCATT	ATGAGATCAT	ATATTCTGTC	TGACCTTATT	480
	ATGTAATTC	ACAAATAAAA	ACTTTTATAT	TATTTATTTG	TAACCTAAAT	AGAATTGGAA	540
	AGATAAGGGT	AATTATGAAA	TTACCCATAT	CATAGTTTTT	TATAAAGTTA	ATAAATAATA	600
	TTTTATCCCT	GTAATAAGCA	GGTATTTGTa	ataaacttga	catgagtcac	agaacattag	660
	atatctttag						670
				--0.2 kb--			
<u>XbaI</u>	tccatctgct	gctgcctggc	tatttctctc	aatcgattct	gtgacatttc	acttctagaa	060
	gagcaGCTAT	AATCCAAGCC	TAAGAAGTAA	TTTTATTTAT	TTATTATTTT	TTCTTTTATA	120
	ATATGTGCTT	CTTACCAGTC	AAAAAGTATT	ATAAACTATT	AGAAAAGAAA	ATCTAAAGGT	180
	AGAAATTTTA	AAATTCAATT	AACAAGTAAA	TTTTACTTTT	TTTTTTTTTT	TTTTTTTTTT	240
EXON 22	ACTGTTCTTC	CTCAGACATT	CAACGTGTT	TTGATCAAAG	AAGAGGAGTA	TGATTCTATT	300
		ThrPh	eLysArgVal	LeuIleLysG	luGluGluTy	rAspSerIle	(752)
	ATAGTATTCT	ATAACTCGGT	CTTCATGCAG	AGACTGAAAA	CAAATATTTT	GCAGTATGCT	360
	IleValPheT	yrAsnSerVa	lPheMetGln	ArgLeuLysT	hrAsnIleLe	uGlnTyrAla	(772)
	TCCACCAGGG	TAGGTCAAAA	GTATCCTTTG	ATTGGAAAAA	TCTAATGTAA	TGGGTCCACC	420
	SerThrArg						(775)
EXON 23	AAAACATTAA	ATAAATAATC	TACTTTTTTG	TTTTTGCTCT	AGCCCCCTAC	CTTGTCACCA	480
					ProProTh	rLeuSerPro	(781)
	ATACCTCACA	TTCTCGAAG	CCCTTACAAG	TTTCCTAGTT	CACCCTTACG	GATTCTTGGA	540
	IleProHisI	leProArgSe	rProTyrLys	PheProSerS	erProLeuAr	gIleProGly	(801)
	GGGAACATCT	ATATTTCAAC	CCTGAAGAGT	CCATATAAAA	TTTCAGAAGG	TCTGCCAACA	600
	GlyAsnIleT	yrIleSerPr	oLeuLysSer	ProTyrLysI	leSerGluGl	yLeuProThr	(821)
	CCAACAAAAA	TGACTCCAAG	ATCAAGGTGT	GTGTTTTCTC	TTTAGGGAAG	TAGTAAAGAA	660
	ProThrLysH	etThrProAr	gSerAr				(830)
	TGAGAGGGGG	ATTATTTTGA	TCCAAGAATA	AAAAATATAA	AGCATTCTTC	ATTTCAAATA	720
	AGCTAGACTC	TTGAAACTCT	ATTTGCTTAT	TTAAGTAACA	TAATAAGAAT	ATGGGGGCGG	780
	GGTGAAGAAA	ATCTATTTAC	GACTTAAGCA	ACGCAAGATG	GCCGAATAGG	AACAGCTCCg	840
	gtctacagct	cccagegtga	gcacgcagaa	gacgggtgat	ttctgcattt	ccatctgagg	900
	taccgggttc	atctcactag	ggagtgccag	acagt			935
				--7.4 kb--			
	ttgataactt	accatttgat	ttatgaagaa	ctaagtaggg	gtaaccttga	aacttgcttt	060
	tgccttccct	aatatgggc	aatggcagna	tatgttcttg	cagacctata	acttttgctT	120
	TAAAACTAAG	AGACTAGGTG	AGTATATGAT	TAGACGGGCA	CTGTTAGAAT	AATTTCCAAA	180
	TGAATATAGT	TTGTCAGTGG	TTCTAGGGTA	GAGGTAACCT	TTAATTTGGT	ATTCCTAATA	240
	GTTTCAAGATG	ATGTATTTAT	GCTCATCTCT	GCAAAATTGT	ATATGGTTTT	TTATTACTAA	300
EXON 24	TTGGTATTTT	ATCTTAACTT	GACAGAATCT	TAGTATCAAT	TGGTGAATCA	TTGGGGGTGA	360
			gIleL	euValSerIl	eGlyGluSer	PheGly	(840)
<u>HindIII</u>	GTATTTTCTT	TCTATGAAAT	ATAATAGTAT	GCATTGTAAG	TATAAAAGAA	ATTAAGCTT	420
	TCTATAATTT	GAATTTCCAA	ATGCAGTTAT	TCAAACACCT	CATCCAGGCA	TATTGCATAG	480
	AATTTTATGA	GATATATATA	TCTCAGATTT	ACTTTCAAAT	CAAGTTTAAT	CTCAAATCAT	540
	ACTCCTAATT	GGTGAACITC	AAAACTTTTC	TAAATATCCA	CTTGAGATTA	TATAATACAT	600
	ATATACATTT	GTGTATATAT	ATACATATAT	ACGTGAGCTG	TTTTTGCTCA	CAACATTTCT	660
	ATCACCAAAT	GTGTGAGATT	TTTTTCTCAC	CCAAATCTAT	TCTTcaactc	tctggtgctt	720
	ctacaattca	attcaattct	gacactaatt	accagag			758
				--2.8 kb--			

FIG. 6-8

	gggatggaa	ttaggtagtt	attctgattt	ttAGATTTT	CATATCTTTT	ATTGGTCCA	060
	ATGAAGCAGA	AAATTTAAAT	GAAGTTATTA	CCTTTGCCGTG	ATTTTGGACA	CACCTCAAAC	120
<u>EcoRI</u>	TATAACTTGA	GGTTGCTAAC	TATGAAACAC	TGGCATTIAA	TGATTTAAAG	TAAAGAATTC	180
EXON 25	TGTAATTTGT	AGACTTCTGA	GAAGTTCAG	AAAATAAATC	AGATGGTATG	TAACAGCCGAC	240
	ThrSerG1 uLysPheGln LysIleAsnG lnMetValCy sAsnSerAsp (856)						
	CGTGTGCTCA	AAAGAAGTGC	TGAAGGAAGC	AACCCTCCTA	AACCACTGAA	AAAACCTACGC	300
	ArgValLeuL	ysArgSerAl	aGluGlySer	AsnProProL	ysProLeuLy	sLysLeuArg	(876)
	TTTGATATTG	AAGGATCAGA	TGAAGCAGAT	GGAAGGTAGG	AACCAGTTTT	GAATGTTTTTC	360
	PheAspIleG	luGlySerAs	pGluAlaAsp	GlySe			(888)
	CAGTAGCTGA	GATGGTCATC	TGGGGAATCC	AGAGTCTCAG	CACTGCTCCT	GGCTTATACC	420
	AATTTCTTTC	ATGCCAAGTT	TATTTGGAAG	TTGTGAGAAT	GGCTCAAAAT	AATAGATATG	480
	AGTGTAGTGC	AAAGTTAAAA	ACATCTTACA	AATTGCATAC	CAACATTCAG	TGAAGATATC	540
	TAATAAACCC	TGATCTTTTT	TACAAAGCTA	TTGATAAAAT	TTTGTATTTC	TTAACATTAA	600
	ATTTAAAAAT	GTTTACTCTT	GAAAAATATT	AACCACTGTA	TTTTGTGAGA	ACCACTGAAA	660
	AAATACATAG	CATCATAAAT	TTGTGACATT	TATGTTTTAG	ATGGTTAGTT	TTTAAATTTT	720
	AAAATTAATA	GCTACTCACT	AAAATAATAG	CATAAAGTAA	GTCATCGAAA	GCATCATAGT	780
	TACTGGAAAT	TTGAGTTTTT	CATTTATAAA	TACACATGAA	ATGTTTTGCA	TTTTTTTAAAT	840
EXON 26	CTGCAGTAAA	CATCTCCCAG	GAGAGTCCAA	ATTCAGCAG	AACTGGGCAG	AAATGAGTAA	900
	rLys HisLeuProG lyGluSerLy sPheGlnGln LysLeuAlaG luMetT (905)						
	GTACTTTTTT	CACCTTGTGT	AAACGAAATA	AACAATTGTT	TACACTGCAA	GAAGTCTTTT	960
	CGTTATATAA	AAGAATGTAT	AATTTCTTCA	GTTGGCAGGT	TTGTTTATGC	ATTTAAAAATA	1020
	TAATTCAATC	AAGGTTATTT	ATCTACAAAC	ATTTGTGGAT	TAAATGTATG	ATGTAAAAATG	1080
	AAGGTCATTT	TTACCCTTTC	TATGATCTTT	CATGCAGGAA	GACTAAGAAG	TGAAACATTG	1140
	CTTGACCACA	TTCAAcacaa	atggctacag	ttagaaaata	cttttagcaga	actacaaaaga	1200
	ggaactatTT	gggagtgtta	gatataggga	aaagtTTTtat	aaacctagca	tatgtaaaac	1260
	atcatcaccc	ttatttaagg	aataaccttt	gattctaccg	atTTTTaaac		1310
	--1.7 kb--						
	tctagctatt	tgaatatgca	gtaaattaac	tgtaactcct	acgggtactgt	caaatactag	060
	aatgaagacc	acctctTTTT	gcAAGGTCC	GAGCGCCATC	AGTTTGACAT	GAGCATAATA	120
	TATATGGCAG	CCACTTGCCA	ACTTACCCAG	TACCATCAAT	GCTGTTAACA	GTTCTTCATC	180
EXON 27	CTTTTCCAG	CTTCTACTCG	AACACGAATG	CAAAAGCAGA	AAATGAATGA	TAGCATGGAT	240
	hrSerThrAr gThrArgMet GlnLysGlnL ysMetAsnAs pSerMetAsp (921)						
	ACCTCAAACA	AGGAAGAGAA	ATGAGGATCT	CAGGACCTTG	GTGGACACTG	TGTACACCTC	300
	ThrSerAsnL	ysGluGluLy	sEND 3	untranslated region begins here (928)			
	TGGATTCAAT	GTCTCTCACA	GATGTGACTG	TATAACTTTC	CCAGGTTCTG	TTTATGGCCA	360
	CATTTAATAT	CTTCAGCTCT	TTTTGTGGAT	ATAAAATGTG	CAGATGCAAT	TGTTTGGGTG	420
	ATTCCTAAGC	CACTTGAAAT	GTTAGTCATT	GTTATTTATA	CAAGATTGAA	AATCTTGTGT	480
	AAATCCTGCC	ATTTAAAAAG	TTGTAGCAGA	TTGTTTCCTC	TTCCAAAGTA	AAATTGCTGT	540
	GCTTTATGGA	TAGTAAGAAT	GGCCCTAGAG	TGGGAGTCCT	GATAACCCAG	GCCTGTCTGA	600
	CTACTTTGCC	TTCTTTTGTA	GCATATAGGT	GATGTTTGCT	CTTGTTTTTA	TTAATTTATA	660
	TGTATATTTT	TTTAATTTAA	CATGAACACC	CTTAGAAAAT	GTGTCCTATC	TATCTTCCAA	720
	ATGCAATTTG	ATTGACTGCC	CATTCACCAA	AATTATCCTG	AACCTTCTG	CAAAAATGGA	780
	TATTATTAGA	AATTAGAAAA	AAATTACTAA	TTTACACAT	TAGATTTTAT	TTTACTATTG	840
	GAATCTGATA	TACTGTGTGC	TTGTTTTATA	AAATTTTGCT	TTTAATTAAA	TAAAAGCTGG	900
	AAGCAAAGTA	TAACCATATG	ATACTATCAT	ACTACTGAAA	CAGATTTTAT	ACCTCAGAAT	960
	GTAAAAGAAC	TTACTGATTA	TTTCTTCAT	CCAACCTATG	TTTTTAAATG	AGGATTATTG	1020
	ATAGTACTCT	TGGTTTTTAT	ACCATTGAGA	TCAGTGAATT	TATAAAGTAC	CCATCTAGTA	1080
	CTTGAAAAAG	TAAAGTGTTT	TGCCAGATCT	TAGGTATAGA	GGACCCTAAC	ACAGTATATC	1140
	CCAAGTGAC	TTTCTAATGT	TTCTGGGTCC	TGAAGAAATTA	AGATACAAAT	TAATTTTACT	1200
	CCATAAACAG	ACTGTAAATT	ATAGGAGCCT	TAATTTTTTT	TTTATAGAGA	TTTGTCTAAT	1260
	TGCATCTCAA	AATTATTCTG	CCCTCCTTAA	TTTGGGAAGG	TTTGTGTTTT	CTCTGGAATG	1320
	GTACATGTCT	TCCATGTATC	TTTTGAACTG	GCAATTGTCT	ATTTATCTTT	TATTTTTTTA	1380
	AGTCAGTATG	GTCTAACACT	GGCATGTTCA	AAGCCACATT	ATTTCTAGTC	CAAAATTACA	1440
<u>HindIII</u>	AGTAATCAAG	GGTCATTATG	GGTTAGGCAT	TAATGTTTCT	ATCTGATTTT	GTGCAAAAGC	1500

FIG. 6-9

EXON 27 TTCAAATTAA AACAGCTGCA TTAGAAAAAG AGGCGCTTCT CCCCTCCCCT ACACCTAAAG 1560
(CONTD) 3' untranslated region (continued)
GTGTATTTAA ACTATCTTGT GTGATTAAGT TATTTAGAGA TGCTGTAAGT TAAAAAGGG 1620
GATATTTAAG GTAGCTTCAG CTAGCTTTTA GGAAATCAC TTTGTCTAAC TCAGAATTAT 1680
TTTTAAAAAG AAATCTGGTC TTGTTAGAAA AAAAAATTTT ATTTTGTGCT CATTTAAGTT 1740
TCAAACCTAC TATTTTGACA GTTATTTTGA TAACAATGAC ACTAGAAAAAC TTGACTCCAT 1800
TTCATCATTG TTTCTGCATG AATATCATAC AAATCAGTTA GTTTTTAGGT CAAGGGCTTA 1860
CTATTTCTGG GTCTTTTGCT ACTAAGTTCA CATTAGAATT AGTGCCAGAA TTTTAGGAAC 1920
TTCAGAGATC GTGTATTGAG ATTTCTTAAA TAATGCTTCA GATATTATTG CTTTATTGCT 1980
TTTTTGATT GGTAAAACT GTACATTTAA AATTGCTATG TTAATTTT CTACAATTAA 2040
TAGTTTGTCT ATTTTAAAAAT AAATTAGTTG TTAAGAGTC TTAATGGTCTG ATGTTGTGTT 2100
polyadenylation signal sequence polyadenylation site
CTTTGTATTA AGTACACTAA TGTTCTCTTT TCTGTCTAGG AGAAGATAGA TAGAAGATAA 2160
CTCTCCTAGT ATCTCATCCA TTCCTAGCCT TTAAGGGGCT CTATATGCTA GAGATTTCCA 2220
AATTTATTTT TTCAGCCCTG ATCTTTTCAC AGAGGTCAAG Gcttttatag ccaacagaac 2280
tcttgattcc tactcccntc tacccaatgt ctccaaatat aaactaaaat caaataaata 2340
aaaatctttt tt 2352

HUMAN RETINOBLASTOMA GENE

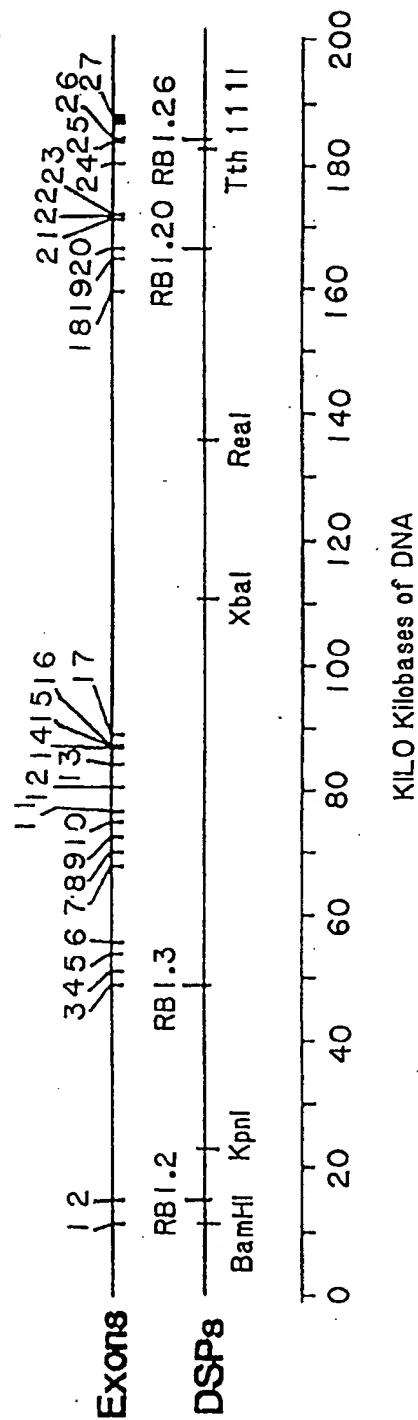


FIG. 8

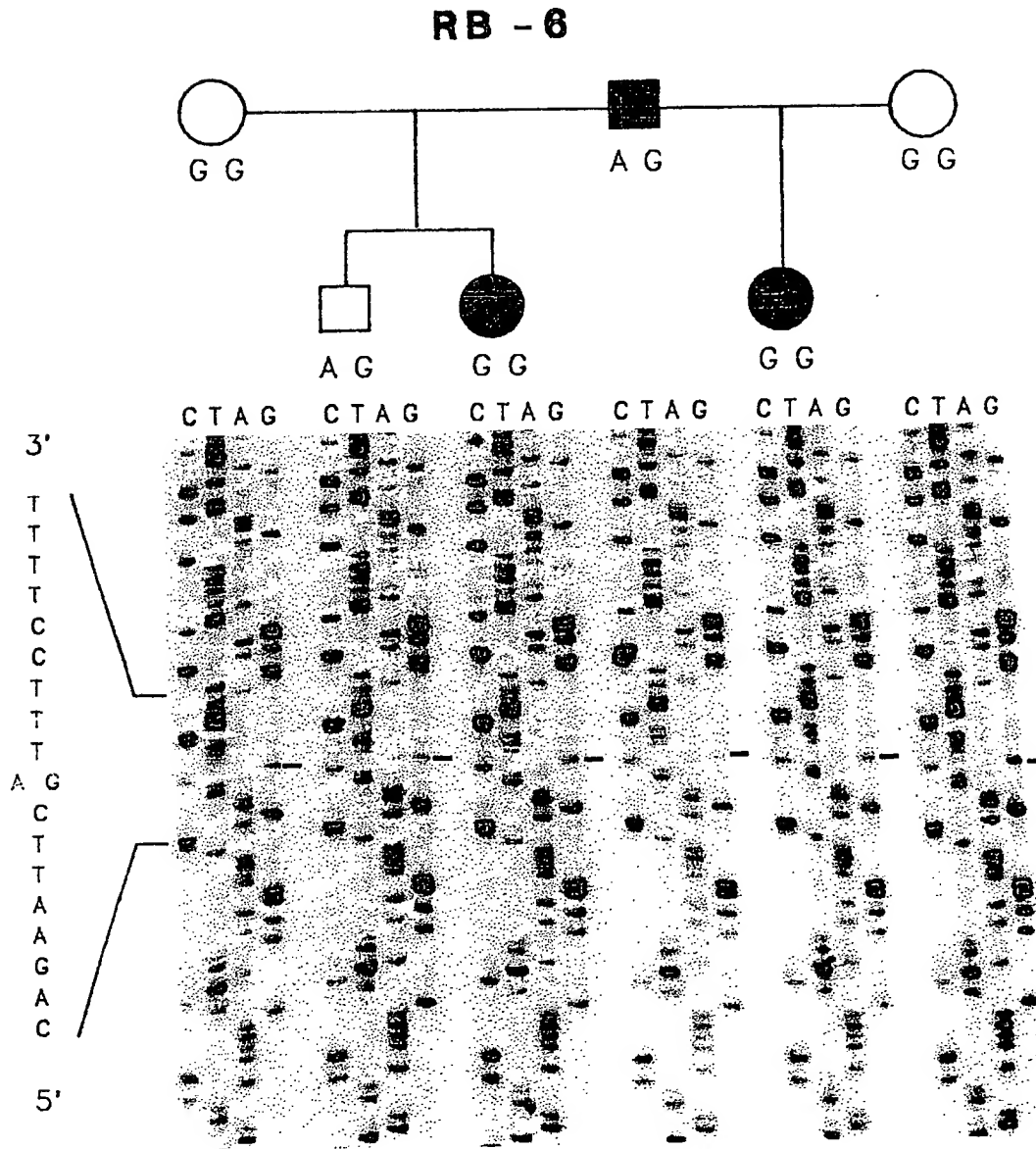
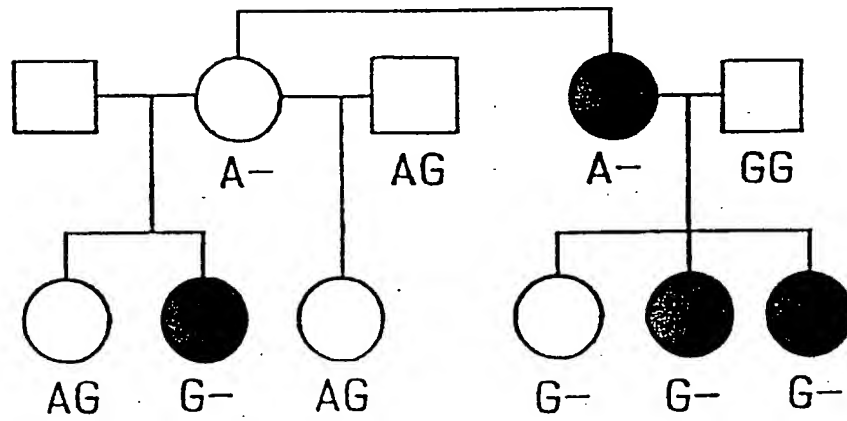
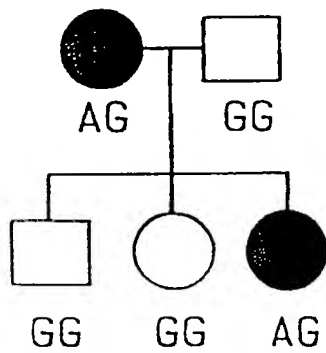


FIG. 9 RB-32



RB-36



RB-50

